

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/541,598  
Source: IFWP  
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IFWP

## RAW SEQUENCE LISTING

DATE: 08/10/2006

PATENT APPLICATION: US/10/541,598

TIME: 09:54:22

Input Set : A:\49321-142 SEQ LIST.txt

Output Set: N:\CRF4\08102006\J541598.raw

3 <110> APPLICANT: Moses, Ashlee  
 4 Frueh, Klaus  
 5 King, Jeffrey S.  
 6 Hicks, James B.  
 7 Raggo, Camilo  
 8 Nelson, Jay  
 10 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS OF KAPOSI'S SARCOMA (KS)  
 AND  
 11 KS RELATED DISEASES  
 13 <130> FILE REFERENCE: 49321-142  
 15 <140> CURRENT APPLICATION NUMBER: US 10/541,598  
 16 <141> CURRENT FILING DATE: 2005-07-05  
 18 <150> PRIOR APPLICATION NUMBER: US 60/438,343  
 19 <151> PRIOR FILING DATE: 2003-01-06  
 21 <150> PRIOR APPLICATION NUMBER: US 60/473,246  
 22 <151> PRIOR FILING DATE: 2003-05-22  
 24 <150> PRIOR APPLICATION NUMBER: PCT US04/00320  
 25 <151> PRIOR FILING DATE: 2004-01-06  
 27 <160> NUMBER OF SEQ ID NOS: 33  
 29 <170> SOFTWARE: PatentIn version 3.3  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 2035  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: homo sapiens  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (152)..(1240)  
 41 <400> SEQUENCE: 1  
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 44 agcgcacagc acagccagga aggcgagcga gccagccag cccagccagc ccagccagcc 120  
 46 cggaggtcat ttgattgccc gcctcagaac g atg gat ctg cat ctc ttc gac 172  
 47 Met Asp Leu His Leu Phe Asp  
 48 1 5  
 50 tac tca gag cca ggg aac ttc tcg gac atc agc tgg cca tgc aac agc 220  
 51 Tyr Ser Glu Pro Gly Asn Phe Ser Asp Ile Ser Trp Pro Cys Asn Ser  
 52 10 15 20  
 54 agc gac tgc atc gtg gtg gac acg gtg atg tgt ccc aac atg ccc aac 268  
 55 Ser Asp Cys Ile Val Val Asp Thr Val Met Cys Pro Asn Met Pro Asn  
 56 25 30 35  
 58 aaa agc gtc ctg ctc tac acg ctc tcc ttc att tac att ttc atc ttc 316  
 59 Lys Ser Val Leu Leu Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe  
 60 40 45 50 55  
 62 gtc atc ggc atg att gcc aac tcc gtg gtg gtc tgg gtg aat atc cag 364  
 63 Val Ile Gly Met Ile Ala Asn Ser Val Val Val Trp Val Asn Ile Gln

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64	60	65	70	
66 gcc aag acc aca ggc tat gac acg cac tgc tac atc ttg aac ctg gcc				412
67 Ala Lys Thr Thr Gly Tyr Asp Thr His Cys Tyr Ile Leu Asn Leu Ala				
68	75	80	85	
70 att gcc gac ctg tgg gtt gtc ctc acc atc cca gtc tgg gtg gtc agt				460
71 Ile Ala Asp Leu Trp Val Val Leu Thr Ile Pro Val Trp Val Val Ser				
72	90	95	100	
74 ctc gtg cag cac aac cag tgg ccc atg ggc gag ctc acg tgc aaa gtc				508
75 Leu Val Gln His Asn Gln Trp Pro Met Gly Glu Leu Thr Cys Lys Val				
76	105	110	115	
78 aca cac ctc atc ttc tcc atc aac ctc ttc ggc agc att ttc ttc ctc				556
79 Thr His Leu Ile Phe Ser Ile Asn Leu Phe Gly Ser Ile Phe Phe Leu				
80 120	125	130	135	
82 acg tgc atg agc gtg gac cgc tac ctc tcc atc acc tac ttc acc aac				604
83 Thr Cys Met Ser Val Asp Arg Tyr Leu Ser Ile Thr Tyr Phe Thr Asn				
84	140	145	150	
86 acc ccc agc agc agg aag aag atg gta cgc cgt gtc gtc tgc atc ctg				652
87 Thr Pro Ser Ser Arg Lys Lys Met Val Arg Arg Val Val Cys Ile Leu				
88	155	160	165	
90 gtg tgg ctg ctg gcc ttc tgc gtg tct ctg cct gac acc tac tac ctg				700
91 Val Trp Leu Leu Ala Phe Cys Val Ser Leu Pro Asp Thr Tyr Tyr Leu				
92	170	175	180	
94 aag acc gtc acg tct gcg tcc aac aat gag acc tac tgc cgg tcc ttc				748
95 Lys Thr Val Thr Ser Ala Ser Asn Asn Glu Thr Tyr Cys Arg Ser Phe				
96	185	190	195	
98 tac ccc gag cac agc atc aag gag tgg ctg atc ggc atg gag ctg gtc				796
99 Tyr Pro Glu His Ser Ile Lys Glu Trp Leu Ile Gly Met Glu Leu Val				
100 200	205	210	215	
102 tcc gtt gtc ttg ggc ttt gcc gtt ccc ttc tcc att atc gct gtc ttc				844
103 Ser Val Val Leu Gly Phe Ala Val Pro Phe Ser Ile Ile Ala Val Phe				
104	220	225	230	
106 tac ttc ctg ctg gcc aga gcc atc tcg gcg tcc agt gac cag gag aag				892
107 Tyr Phe Leu Leu Ala Arg Ala Ile Ser Ala Ser Ser Asp Gln Glu Lys				
108	235	240	245	
110 cac agc agc cgg aag atc atc ttc tcc tac gtg gtg gtc ttc ctt gtc				940
111 His Ser Ser Arg Lys Ile Ile Phe Ser Tyr Val Val Val Phe Leu Val				
112	250	255	260	
114 tgc tgg ctg ccc tac cac gtg gcg gtg ctg ctg gac atc ttc tcc atc				988
115 Cys Trp Leu Pro Tyr His Val Ala Val Leu Leu Asp Ile Phe Ser Ile				
116	265	270	275	
118 ctg cac tac atc cct ttc acc tgc cgg ctg gag cac gcc ctc ttc acg				1036
119 Leu His Tyr Ile Pro Phe Thr Cys Arg Leu Glu His Ala Leu Phe Thr				
120 280	285	290	295	
122 gcc ctg cat gtc aca cag tgc ctg tcg ctg gtg cac tgc tgc gtc aac				1084
123 Ala Leu His Val Thr Gln Cys Leu Ser Leu Val His Cys Cys Val Asn				
124	300	305	310	
126 cct gtc ctc tac agc ttc atc aat cgc aac tac agg tac gag ctg atg				1132
127 Pro Val Leu Tyr Ser Phe Ile Asn Arg Asn Tyr Arg Tyr Glu Leu Met				
128	315	320	325	

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130 aag gcc ttc atc ttc aag tac tgc gcc aaa aca ggg ctc acc aag ctc      1180
131 Lys Ala Phe Ile Phe Lys Tyr Ser Ala Lys Thr Gly Leu Thr Lys Leu
132      330      335      340
134 atc gat gcc tcc aga gtc tca gag acg gag tac tct gcc ttg gag cag      1228
135 Ile Asp Ala Ser Arg Val Ser Glu Thr Glu Tyr Ser Ala Leu Glu Gln
136      345      350      355
138 agc acc aaa tga tctgccctgg agaggctctg ggacggggtt acttggtttt      1280
139 Ser Thr Lys
140 360
142 gaacaggggtg atgggcccta tggttttcta gagcaaagca aagtagcttc ggggtcttgat      1340
144 gcttgagtag agtgaagagg ggagcacgtg cccctgcat ccattctctc tttctcttga      1400
146 tgacgcagct gtcatttggc tgtgcgtgct gacagttttg caacaggcag agctgtgtcg      1460
148 cacagcagtg ctgtgcgtca gagccagctg aggacaggct tgcctggact tctgtaagat      1520
150 aggattttct gtgtttcctg aattttttat atgggtgattt gtattttaaatt ttttaagactt      1580
152 tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat attttaaata      1640
154 ttgtttggga ggcatagtgc tgacatatat tcagagtgtt gtagttttta ggtttagcgtg      1700
156 acttcagttt tgactaagga tgacactaat tgtttagctgt tttgaaatta tatatatata      1760
158 aatatatata aatatataaa tatatgccag tcttggtcga aatgttttat ttaccatagt      1820
160 tttatatctg tgtggtgttt tgtaccggca cgggatatgg aacgaaaact gctttgtaat      1880
162 gcagtttgat acattaatag tattgtaaag ttacatttta aaataaacia aaaactgttc      1940
164 tggactgcaa atctgcacac acaacgaaca gttgcatttc agagagttct ctcaatttgt      2000
166 aagttatttt tttttaataa agatttttgt ttcct      2035
169 <210> SEQ ID NO: 2
170 <211> LENGTH: 362
171 <212> TYPE: PRT
172 <213> ORGANISM: homo sapiens
174 <400> SEQUENCE: 2
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177 1      5      10      15
180 Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
181      20      25      30
184 Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
185      35      40      45
188 Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
189      50      55      60
192 Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
193 65      70      75      80
196 Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
197      85      90      95
200 Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
201      100      105      110
204 Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
205      115      120      125
208 Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
209      130      135      140
212 Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
213 145      150      155      160
216 Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
217      165      170      175

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220 Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
221      180      185      190
224 Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
225      195      200      205
228 Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
229      210      215      220
232 Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
233 225      230      235      240
236 Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser
237      245      250      255
240 Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
241      260      265      270
244 Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
245      275      280      285
248 Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
249      290      295      300
252 Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
253 305      310      315      320
256 Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
257      325      330      335
260 Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
261      340      345      350
264 Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
265      355      360
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1421
270 <212> TYPE: DNA
271 <213> ORGANISM: homo sapiens
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION: (115)..(1092)
278 <400> SEQUENCE: 3
279 ggcgagggag gaggaagaag cggaggaggc ggctcccgcg ctccgagggc cgtgccacct      60
281 gcccgccgcg ccgctcgctc gctcgccgcg cgcgccgcgc tgccgaccgc cagc atg      117
282      Met
283      1
285 ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg ccg ccg ctg      165
286 Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro Leu
287      5      10      15
289 ctg ccg ctg ctg ctg ctg cta ctg ggc gcg agt ggc ggc ggc ggc ggc      213
290 Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Ser Gly Gly Gly Gly Gly
291      20      25      30
293 gcg cgc gcg gag gtg ctg ttc cgc tgc ccg ccc tgc aca ccc gag cgc      261
294 Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr Pro Glu Arg
295      35      40      45
297 ctg gcc gcc tgc ggg ccc ccg ccg gtt gcg ccg ccc gcc gcg gtg gcc      309
298 Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro Ala Ala Val Ala
299 50      55      60      65
301 gca gtg gcc gga ggc gcc cgc atg cca tgc gcg gag ctc gtc cgg gag      357

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302 Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu Leu Val Arg Glu
303          70          75          80
305 ccg ggc tgc ggc tgc tgc tgc gtg tgc gcc cgg ctg gag ggc gag gcg      405
306 Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu Glu Gly Glu Ala
307          85          90          95
309 tgc ggc gtc tac acc ccg cgc tgc ggc cag ggg ctg cgc tgc tat ccc      453
310 Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu Arg Cys Tyr Pro
311          100         105         110
313 cac ccg ggc tcc gag ctg ccc ctg cag gcg ctg gtc atg ggc gag ggc      501
314 His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val Met Gly Glu Gly
315          115         120         125
317 act tgt gag aag cgc cgg gac gcc gag tat ggc gcc agc ccg gag cag      549
318 Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser Pro Glu Gln
319 130          135          140          145
321 gtt gca gac aat ggc gat gac cac tca gaa gga ggc ctg gtg gag aac      597
322 Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu Val Glu Asn
323          150         155         160
325 cac gtg gac agc acc atg aac atg ttg ggc ggg gga ggc agt gct ggc      645
326 His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly Ser Ala Gly
327          165         170         175
329 cgg aag ccc ctc aag tgc ggt atg aag gag ctg gcc gtg ttc cgg gag      693
330 Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val Phe Arg Glu
331          180         185         190
333 aag gtc act gag cag cac ccg cag atg ggc aag ggt ggc aag cat cac      741
334 Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly Lys His His
335          195         200         205
337 ctt ggc ctg gag gag ccc aag aag ctg cga cca ccc cct gcc agg act      789
338 Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro Ala Arg Thr
339 210          215          220          225
341 ccc tgc caa cag gaa ctg gac cag gtc ctg gag cgg atc tcc acc atg      837
342 Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile Ser Thr Met
343          230         235         240
345 cgc ctt ccg gat gag cgg ggc cct ctg gag cac ctc tac tcc ctg cac      885
346 Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr Ser Leu His
347          245         250         255
349 atc ccc aac tgt gac aag cat ggc ctg tac aac ctc aaa cag tgc aag      933
350 Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys Gln Cys Lys
351          260         265         270
353 atg tct ctg aac ggg cag cgt ggg gag tgc tgg tgt gtg aac ccc aac      981
354 Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val Asn Pro Asn
355          275         280         285
357 acc ggg aag ctg atc cag gga gcc ccc acc atc cgg ggg gac ccc gag      1029
358 Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly Asp Pro Glu
359 290          295          300          305
361 tgt cat ctc ttc tac aat gag cag cag gag gct cgc ggg gtg cac acc      1077
362 Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly Val His Thr
363          310         315         320
365 cag cgg atg cag tag accgcagcca gccggtgcct ggcgccctg ccccccgcgc      1132
366 Gln Arg Met Gln

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